



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
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(E) COUNTRY: US
(F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 7.0.1
(D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: -to be assigned-
(B) FILING DATE: December 3, 1993
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/111,758
(B) FILING DATE: August 25, 1993
(C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/106,463
(B) FILING DATE: August 12, 1993
(C) CLASSIFICATION:
- (ix) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 2813-C
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..25

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 855..879

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGCACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG GCAGAG	56
ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG	104
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu	
1 5 10 15	
CTG TTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC	152
Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr	
20 25 30	
TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG	200
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu	
35 40 45	
TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT	248
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn	
50 55 60	
CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC	296
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala	
65 70 75 80	
CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA	344
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln	
85 90 95	
ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT	392
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys	
100 105 110	
ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC	440
Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile	
115 120 125	
TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC	488
Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro	
130 135 140	

TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln 145 150 155 160	536
TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala 165 170 175	584
CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu 180 185 190	632
CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Ala Ala Ala Trp 195 200 205	680
GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly 210 215 220	728
GTG CCC CTC CCC TCC CAT CCC TAGGATTGCA GCCTTGCA TCGTTGACTC Val Pro Leu Pro Ser His Pro 225 230	779
AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT 839	
TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC	879

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu 1 5 10 15
Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr 20 25 30
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu 35 40 45
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn 50 55 60
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala 65 70 75 80
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln 85 90 95
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys 100 105 110

Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
115 120 125

Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
130 135 140

Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
145 150 155 160

Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
165 170 175

Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
180 185 190

Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
195 200 205

Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
210 215 220

Val Pro Leu Pro Ser His Pro
225 230

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 988 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT	TCCGGGGCCC	CCGGCCGAA	ATG	ACA	GTG	CTG	GCG	CCA	GCC	TGG	53
			Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	
			1						5		
AGC	CCA	ACA	ACC	TAT	CTC	CTC	CTG	CTG	CTG	CTG	101
Ser	Pro	Thr	Thr	Tyr	Leu	Leu	Leu	Leu	Leu	Ser	
10					15				20		
AGT	GGG	ACC	CAG	GAC	TGC	TCC	TTC	CAA	CAC	AGC	149
Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	
25					30				35		
TTC	GCT	GTC	AAA	ATC	CGT	GAG	CTG	TCT	GAC	TAC	197
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	
				45				50		55	
CCA	GTC	ACC	GTG	GCC	TCC	AAC	CTG	CAG	GAC	GAG	245
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	
				60				65		70	
CTC	TGG	CGG	CTG	GTC	CTG	GCA	CAG	CGC	TGG	ATG	293
Leu	Trp	Arg	Leu	Val	Ala	Gln	Arg	Trp	Met	Glu	
				75			80			85	
GTC	GCT	GGG	TCC	AAG	ATG	CAA	GGC	TTG	CTG	GAG	341
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	
				90			95			100	
ATA	CAC	TTT	GTC	ACC	AAA	TGT	GCC	TTT	CAG	CCC	389
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	
				105			110			115	
CGC	TTC	GTC	CAG	ACC	AAC	ATC	TCC	CGC	CTC	CTG	437
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	
				125				130			135
CAG	CTG	GTG	GCG	CTG	AAG	CCC	TGG	ATC	ACT	CGC	485
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	
				140				145			150
TGC	CTG	GAG	CTG	CAG	TGT	CAG	CCC	GAC	TCC	TCA	533
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	
				155				160			165

TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro	170	175	180	581
CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC Pro Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala	185	190	195	200
GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg	205	210	215	677
CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu	220	225	230	725
GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC Val Glu His	235			774
GCAGTGAGAC AGACATCTAT CATCCCCATT TACAGGGGAG GATACTGAGG CACACAGAGG	834			
GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC	894			
CCTTCCTTGG GCCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC	954			
GGCCCCATTT ACCCAAATCT GAACAAAGCC CCCG	988			

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
   1           5           10          15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
   20          25          30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
   35          40          45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
   50          55          60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
   65          70          75          80

Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
   85          90          95

Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
  100         105         110

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Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu
 180 185 190
 Pro Val Gly Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
 195 200 205
 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
 210 215 220
 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
 225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60
 ACTTCAGCCA C 71

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37